

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.						
Result No.	Score	Query Match	Length	DB ID	Description	
c 1	13.4	60.9	41	6 A93667	A93667 Sequence 3	A9881 Sequence 9
c 2	13	59.1	37	6 A9881	A9881 Sequence 9	A9881 Sequence 9
c 3	12.8	58.2	35	6 AR059842	AR059842 Sequence	S5733 T-cell-rece
c 4	12.8	58.2	57	9 S57433	S5733 T-cell-rece	S5733 T-cell-rece
c 5	12.6	57.3	37	6 A9888	A9888 Sequence 6	A9888 Sequence 6
c 6	12.6	57.3	48	3 HCUB4A86	HCUB4A86 Haemophilus	U84186 Haemophilus
c 7	12.6	57.3	58	6 118948	118948 Sequence 30	118948 Sequence 30
c 8	12.6	57.3	58	6 118949	118949 Sequence 31	118949 Sequence 31
c 9	12.6	57.3	58	6 124133	124133 Sequence 30	I24134 Sequence 30
c 10	12.6	57.3	58	6 124134	I24134 Sequence 31	I24134 Sequence 31
c 11	12.4	56.4	40	6 AR15048	AR15048 Sequence	AR15048 Sequence
c 12	12.4	56.4	42	6 AR12052	AR12052 Sequence	AR12052 Sequence
c 13	12.4	56.4	51	6 AX118585	AX118585 Sequence	AX118585 Sequence
c 14	12.2	55.5	27	6 AR153624	AR153624 Sequence	AR153624 Sequence
c 15	12.2	55.5	51	6 AR2067	AR2067 Sequence	A42057 Sequence
c 16	12.2	55.5	51	6 AX160849	AX160849 Sequence	AX160849 Sequence
c 17	12.2	55.5	60	6 A80463	A80463 Sequence	A80463 Sequence
c 18	12	54.5	31	6 140626	140626 Sequence 3	140626 Sequence 3
c 19	12	54.5	49	6 108645	108645 Sequence 1	I108645 Sequence 1
c 20	12	54.5	51	9 578430	578430 Homo sapien	578430 Homo sapien
c 21	12	54.5	57	9 HSTRK6X35	H.sapiens mm	Z69556 H.sapiens mm
c 22	12	54.5	57	9 HSTRK6X36	H.sapiens mm	Z69569 H.sapiens mm
c 23	12	54.5	57	9 HSTRKX13	H.sapiens mm	Z69570 H.sapiens mm
c 24	12	54.5	57	9 HSTRKX35	H.sapiens mm	Z69578 H.sapiens mm
c 25	12	54.5	57	9 HSTRKX36	H.sapiens mm	Z69582 H.sapiens mm
c 26	12	54.5	57	9 HSTRKX36	H.sapiens mm	Z69585 H.sapiens mm
c 27	11.8	53.6	26	6 179834	179834 Sequence 19	AR05995 Sequence 19
c 28	11.8	53.6	32	6 AR054995	AR054995 Sequence	AR054995 Sequence
c 29	11.8	53.6	32	6 AR15644	AR15644 Sequence	AR15644 Sequence
c 30	11.8	53.6	20	6 AR129487	AR129487 Sequence	AR129487 Sequence
c 31	11.6	52.7	20	6 E31432	E31432 Gene parbic	E31432 Gene parbic
c 32	11.6	52.7	27	6 AR008922	AR008922 Sequence	AR008922 Sequence
c 33	11.6	52.7	27	6 AR087617	AR087617 Sequence	AR087617 Sequence
c 34	11.6	52.7	28	6 182037	182037 Sequence 76	182037 Sequence 76
c 35	11.6	52.7	28	6 186428	186428 Sequence 75	186428 Sequence 75
c 36	11.6	52.7	35	6 191725	191725 Sequence 75	191725 Sequence 75
c 37	11.6	52.7	35	6 A17073	A17073 oligonucleo	A17073 oligonucleo
c 38	11.6	52.7	35	6 A17074	A17074 oligonucleo	A17074 oligonucleo
c 39	11.6	52.7	35	6 A17471	A17471 oligonucleo	A17471 oligonucleo
c 40	11.6	52.7	35	6 A17472	A17472 oligonucleo	A17472 oligonucleo
c 41	11.6	52.7	35	6 A23883	A23883 oligonucleo	A23883 oligonucleo
c 42	11.6	52.7	35	6 A23899	A23899 oligonucleo	A23899 oligonucleo
c 43	11.6	52.7	35	6 AR014441	AR014441 Sequence	AR014441 Sequence
c 44	11.6	52.7	35	6 AR014450	AR014450 Sequence	AR014450 Sequence
c 45	11.6	52.7	35	6 AR059828	AR059828 Sequence	AR059828 Sequence
ALIGNMENTS						
RESULT 1						
A93667/c						
LOCUS	A93667		41 bp	DNA		
DEFINITION		Sequence 3	from Patent	WO9734144.	PAT	22-JAN-2000
ACCESSION	A93667					
VERSION	A93667.1		G1:6741855			
KEYWORDS						
SOURCE		synthetic construct.				
ORGANISM		synthetic construct.				
REFERENCE	1 (bases 1 to 41)	artificial sequence.				
AUTHORS	Langer, G. and Toschi L.					
TITLE	METHOD OF DETECTING THE EFFECT OF TEST SUBSTANCES USING HEN					
FEATURES	JOURNAL	UROKINASE	Patent: WO 9734144-A 3 18-SEP-1997;			
		SCHERING AG (DE); LANGER GERNOT (DE)	Location; qualifiers			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	BASE COUNT	5 a	14 c	15 g	7 t	ORIGIN
Query Match		60.9%	Score 13.4;	DB 6;	Length 41;	
Best Local Similarity		93.3%	Pred. No. 1.6e+04;			
Matches	14;	Conservative	0;	Mismatches	1;	Indels
Qy	1	cacccgtcttcgtca 15				
Db	31	CACCGCTTCCTGA 17				
RESULT	2					
A98891	A98891	37 bp	DNA			
LOCUS	Sequence 9 from Patent WO9909211.					
DEFINITION						
ACCESSION	A98891					
VERSION	A98891.1	GI:6781850				
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 37)					
AUTHORS	Coutts,J.C. and Oultram,J.D.					
JOURNAL	Patent: WO 9909211-A 9 25 FEB 1999;					
COURTS	JACQUELINE CLARE (GB); OULTRAM JOHN DOUGLAS (GB)					
FEATURES	Location/Qualifiers					
SOURCE	1. .37					
AMPLIFICATION	NUCLEIC ACIDS					
TITLE	/db_xref="taxon;32644"					
BASE COUNT	9 a	8 c	9 g	11 t		
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Best Local Similarity		76.2%	Pred. No. 2.7e+04;			
Matches	16;	Conservative	0;	Mismatches	5;	Indels
Qy	2	acccgtcttcgtacaatgga 22				
Db	8	ANCCACTCTCTGAGGGTGA 28				
RESULT	3					
AR059842/C	AR059842	35 bp	DNA			
LOCUS	Sequence 50 from patent US 5840521.					
DEFINITION						
ACCESSION	AR059842					
VERSION	AR059842.1	GI:5986292				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 35)					
AUTHORS	Barth,P.Thomas.					
JOURNAL	Expression vector containing an inducible selection gene system					
FEATURES	Patent: US 5840521-A 50 24-Nov-1998;					
SOURCE	Location/Qualifiers					
BASE COUNT	10 a	7 c	9 g	9 t		
ORIGIN						
Query Match		58.2%	Score 12.8;	DB 9;	Length 57;	
Best Local Similarity		87.5%	Pred. No. 3.5e+04;			
Matches	14;	Conservative	0;	Mismatches	2;	Indels
Qy	5	cgtcttcgtacatg 20				
Db	1	CCTCTCTGACATGTG 16				
RESULT	5					
A98888	A98888	37 bp	DNA			
LOCUS	Sequence 6 from Patent WO9909211.					
DEFINITION						
ACCESSION	A98888					
VERSION	A98888.1	GI:6781847				
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 37)					
AUTHORS	Coutts,J.C. and Oultram,J.D.					
JOURNAL	AMPLIFICATION OF NUCLEIC ACIDS					
FEATURES	Patent: WO 9909211-A 6 25-FEB-1999;					
SOURCE	Location/Qualifiers					
BASE COUNT	6 a	10 c	10 g	11 t		
Query Match		58.2%	Score 12.8;	DB 6;	Length 35;	
Best Local Similarity		87.5%	Pred. No. 3.4e+04;			
Matches	14;	Conservative	0;	Mismatches	2;	Indels
Qy	6	gtcttcgtacatg 21				
Db	22	GCTCTCTGACATGTG 7				



QY	1	cacccgtctcgacaat	19	LOCUS	AR123052	42 bp	DNA	Sequence 43 from patent US 6168943.	PAT	16-MAY-2001
Db	14	CATCCGCTCTGGCCAAAT	32	DEFINITION	Accession AR123052					
RESULT	10	I24134/c	124134	58 bp	DNA	Sequence 31 from patent US 5543141.	PAT	07-OCT-1996		
LOCUS				DEFINITION	Accession I24134					
DEFINITION				VERSION	AR123052.1	GI:14108018				
ACCESSION				KEYWORDS						
VERSION				SOURCE	Unknown.					
SOURCE				ORGANISM	Unknwn.					
ORGANISM				REFERENCE	Unclassified.					
REFERENCE				AUTHORS	1 (bases 1 to 42)					
REFERENCE				TITLE	Rose,J.K.					
REFERENCE				JOURNAL	Methods for making modified recombinant vesiculoviruses					
FEATURES				FEATURES	Patent: US 6168943-A 07-JAN-2001;					
source				SOURCE	1. .42					
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Matches	78.9%	Pred. No. 4.3e+04;	Length 58;	DEFINITION	72.7%	Pred. No. 5.8e+04;	Length 51;	Length 51;		
OY	1	cacccgtctcgacaat	19	DEFINITION	Accession AR118585	31	Sequence 3708 from Patent WO0129262.	PAT		
Db	49	CATCCGCTCTGGCCAAAT	31	VERSION	AR118585.1	GI:14035536				
RESULT	11	AR150948	AR150948	40 bp	DNA	Sequence 324 from patent US 6229064.	PAT	08-AUG-2001		
DEFINITION				DEFINITION						
ACCESSION				ACCESSION						
VERSION				VERSION						
KEYWORDS				KEYWORDS						
SOURCE				SOURCE	human.					
ORGANISM				ORGANISM	Homo sapiens					
REFERENCE				REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;					
AUTHORS				AUTHORS	Mammalia; Eutheria; Primates; Cetarrhini; Hominidae; Homo.					
TITLE				TITLE	Picoult-Newburg,L. and Pohl,M.					
JOURNAL				JOURNAL	Genotyping reagents, kits and methods of use thereof					
FEATURES				FEATURES	Patent: WO 0129262-A 3708 26-APR-2001;					
source				FEATURES	Orchid Biosciences, Inc. (US)					
BASE COUNT	12	a	11	BASE COUNT	Location/Qualifiers					
ORIGIN			c	ORIGIN	1. .51					
Query Match				Query Match						
Best Local Similarity	56.4%	Score 12.4;	DB 6;	DEFINITION	Best Local Similarity	56.4%	Score 12.4;	DB 6;	Length 51;	
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OY	1	cacccgtctcgacaatggaa	22	DEFINITION	Accession AR153624	27 bp	DNA	Sequence 24 from patent US 6235878.	PAT	08-AUG-2001
Db	4	CATCTTCCTCACCAATGCA	25	VERSION	AR153624.1	GI:15121156				
RESULT	12	ART23052		KEYWORDS						
REFERENCE				SOURCE	Unknown.					
AUTHORS				ORGANISM	Unclassified.					
				REFERENCE	1 (bases 1 to 27)					
				AUTHORS	Nishi,K., Hikichi,Y. and Shintani,Y.					

TITLE Fas ligand-like protein, its production and use  
 JOURNAL Patent: US 6225878 A 24 22-MAY-2001;  
 FEATURES Location/Qualifiers  
 source 1. .27  
 /organism="unknown"  
 BASE COUNT 8 a 9 c 3 g 7 t  
 ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 27;  
 Best Local Similarity 82.4%; Pred. No. 7, 5+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 6 gatcttcgtcggacaatggaa 22  
 ||||| | | | | | | | |  
 Db 26 GCTATGACGACATGGAA 10

RESULT 15  
 A42067/c  
 LOCUS A42067 51 bp DNA  
 DEFINITION Sequence 10 from Patent WO9500637.  
 ACCESSION A42067  
 VERSION A42067.1 GI:2297559  
 KEYWORDS unclassified.  
 SOURCE unclassified.  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 51)  
 AUTHORS Hansson,L.  
 TITLE TRANSGENIC PRODUCTION OF EC-SOD  
 JOURNAL Patent: WO 9500637-A 10 05-JAN-1995;  
 COMMENT SYMBIOM AB (SE) Other publication CA 2164089 950105  
 Other publication AU 6935694 950117.  
 FEATURES Location/Qualifiers  
 source 1. .51  
 /organism="unclassified"  
 CDS /db\_xref="taxon:32644"  
 1. .24  
 /note="Protein sequence is in conflict with the conceptual  
 translation"  
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 /db\_xref=GI:2297560"  
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 BASE COUNT 14 a 19 g 4 t  
 ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 51;  
 Best Local Similarity 82.4%; Pred. No. 7, 5+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 cacccgttcgtcggaca 17  
 ||||| | | | | | | | |  
 Db 38 CACTCGCTCTCGGTCA 22

Search completed: March 9, 2002, 00:48:40  
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